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## SEQUENCE LISTING

&lt;110&gt; Cargill Incorporated

&lt;120&gt; ALANINE 2, 3-AMINOMUTASE

&lt;130&gt; 63358

&lt;150&gt; US 60/350,727

&lt;151&gt; 2002-01-18

&lt;150&gt; US 60/375,785

&lt;151&gt; 2002-04-25

&lt;160&gt; 66

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 40

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 1

gcgcgaggag gagttcatat gaaaaacaaa tggataaac

40

&lt;210&gt; 2

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 2

cgggcaccgc ttcgaggcgg ccgcaccatt cgcatg

36

&lt;210&gt; 3

&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; Bacillus subtilis

&lt;400&gt; 3

ttgaaaaaca aatggtataa accgaaacgg cattggaagg agatcgagtt atggaaggac

60

gttccggaag agaaatggaa cgattggctt tggcagctga cacacactgt aagaacgtta

120

gatgatttaa agaaagtcat taatctgacc gaggatgaag aggaaggcgt cagaatttct

180

acccaaaacga tcccttaaa tattacacct tactatgctt cttaatgga ccccgacaat

240

ccgagatgcc cggtacgcat gcagtcgtg ccgtttctg aagaaatgca caaaacaaaa

300

tacgatctgg aagacccgct tcatgaggat gaagattcac cggtacccgg tctgacacac

360

cgctatcccg accgtgtgct gtttctgtc acgaatcaat gttccatgtc ctggcgctac

420

|             |            |            |             |            |            |      |
|-------------|------------|------------|-------------|------------|------------|------|
| tgcacaagaa  | ggcgctttc  | cgacaaatc  | ggaatggcg   | tcccaaaaa  | acagcttgat | 480  |
| gctgcaattg  | cttatatccg | ggaaacaccc | gaaatcccg   | attgttaat  | ttcaggcggt | 540  |
| gatgggctgc  | tcatcaacga | ccaaattta  | gaatataattt | taaaagagct | gcmcagcatt | 600  |
| ccgcacatcg  | aagtcatcag | aatcggaca  | agagctcccg  | tcgtcttcc  | gcagcgcatt | 660  |
| accgatcatc  | tgtgcgagat | attgaaaaaa | tatcatccgg  | tctggctgaa | cacccattt  | 720  |
| aacacaagca  | tcgaaatgac | agaagaatcc | gttgaggcat  | gtgaaaagct | ggtgaacgcg | 780  |
| ggagtgcgg   | tcggaaatca | ggctgtcgta | ttagcaggtta | ttaatgattc | ggttccaatt | 840  |
| atgaaaaagc  | tcatgcata  | cttggtaaaa | atcagagtcc  | gtccttatta | tatccacaa  | 900  |
| tgtgatctgt  | cagaaggaat | agggcatttc | agagctcctg  | tttccaaagg | tttggagatc | 960  |
| attgaaggc   | tgagaggtca | tacctcaggc | tatgcggttc  | ctaccttgc  | cggtgacgca | 1020 |
| ccaggcggag  | gaggtaaaat | cgcctgcag  | ccaaactatg  | tcctgtcaca | aagtccgtac | 1080 |
| aaagtgtatct | taagaaattt | tgaaggtgtg | attacgtcat  | atccgaaacc | agagaattat | 1140 |
| atccccaaatc | aggcagacgc | ctatttgag  | tccgtttcc   | ctgaaaccgc | tgacaaaaag | 1200 |
| gagccgatcg  | ggctgagtgc | cattttgct  | gacaaagaag  | tttcgtttac | acctgaaaat | 1260 |
| gtagacagaa  | tcaaaaggag | agaggcatac | atcgcaaatc  | cgagcatga  | aacattaaaa | 1320 |
| gatcggcgtg  | agaaaagaga | tcaagctaaa | gaaaagaaaat | tttggcgca  | gcagaaaaaa | 1380 |
| cagaaagaga  | ctgaatgcgg | aggggattct | tcatga      |            |            | 1416 |

|                           |            |            |            |            |            |    |
|---------------------------|------------|------------|------------|------------|------------|----|
| <210> 4                   |            |            |            |            |            |    |
| <211> 60                  |            |            |            |            |            |    |
| <212> DNA                 |            |            |            |            |            |    |
| <213> Artificial Sequence |            |            |            |            |            |    |
| <220>                     |            |            |            |            |            |    |
| <223> PCR primer          |            |            |            |            |            |    |
| <400> 4                   |            |            |            |            |            |    |
| tatcaattcg                | ttacaggcga | tacatggcac | gcttcggcgc | gtgtaggctg | gagctgcttc | 60 |

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|---------------------------|-------------|------------|------------|-------------|------------|----|
| <210> 5                   |             |            |            |             |            |    |
| <211> 60                  |             |            |            |             |            |    |
| <212> DNA                 |             |            |            |             |            |    |
| <213> Artificial Sequence |             |            |            |             |            |    |
| <220>                     |             |            |            |             |            |    |
| <223> PCR primer          |             |            |            |             |            |    |
| <400> 5                   |             |            |            |             |            |    |
| gatgtcgcgg                | ctgggtgagta | accagccgca | gggataacaa | cataatgaata | tcctccttag | 60 |

|         |  |  |  |  |  |  |
|---------|--|--|--|--|--|--|
| <210> 6 |  |  |  |  |  |  |
|---------|--|--|--|--|--|--|

<211> 20  
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<220>  
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ttaccgagca gcgttcagag 20

<210> 7  
<211> 20  
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<220>  
<223> PCR primer

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cacctggcg 20  
tgacaaccat

<210> 8  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 8  
gcggcg 60  
tgaa gttcccaac ccgttctgcc tctcttcttc gtgtaggctg gagctgctc

<210> 9  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 9  
ttacaacgtt 60  
accgggtgtt ctttctcgcc tttcttaaac catatgaata tcctccttag

<210> 10  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 10  
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aaaacaa aatacgatat ggaagacccg ctccatgagg atgaagattc a

<210> 11  
<211> 51

<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 11  
tgaatcttca tcctcatgga gcgggtcttc catatcgat tttgtttgt g 51

<210> 12  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 12  
gaatcaatgt tccgtatact gccgctac 28

<210> 13  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 13  
gtagcggcag tatacggAAC attgattc 28

<210> 14  
<211> 31  
<212> DNA  
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<220>  
<223> PCR primer

<400> 14  
gttcctacct ttgttgtaca cgcaccaggc g 31

<210> 15  
<211> 31  
<212> DNA  
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<220>  
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<210> 16  
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<213> Artificial Sequence

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<223> PCR primer

<220>

<221> misc\_feature

<222> (1)..(23)

<223> y is t/u or c; s is g or c; b is g, c or t/u.

<400> 16  
ttyatyggby tsggbaayat ggg 23

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> misc\_feature

<222> (1)..(20)

<223> y is t/u or c; s is g or c; b is g, c or t/u; w is a or t/u; n is a, c, g or t/u.

<400> 17  
gaygcncncng tbwssggbgg 20

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> misc\_feature

<222> (1)..(21)

<223> y is t/u or c; r is g or a; n is a, c, g or t/u.

<400> 18  
catrtrtrtr caratyttng c 21

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 19

ggtttacgag ggcgagaacg gcttgct

27

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<210> 20
<211> 1416
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1416)
<223>

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atg aaa aac aaa tgg tat aaa ccg aaa cgg cat tgg aag gag atc gag 48
Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu
1 5 10 15

tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag 96
Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
20 25 30

ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat 144
Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
35 40 45

ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc 192
Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
50 55 60

ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat 240
Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
65 70 75 80

ccg aga tgc ccg gta cgc atg cag tct gtg ccg ctt tct gaa gaa atg 288
Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
85 90 95

cac aaa aca aaa tac gat atg gaa gac ccg ctt cat gag gat gaa gat 336
His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp
100 105 110

tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt 384
Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
115 120 125

ctt gtc acg aat caa tgt tcc gtg tac tgc cgc tac tgc aca aga agg 432
Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg
130 135 140

cgc ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat 480
Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
145 150 155 160

gct gca att gct tat atc cgg gaa aca ccc gaa atc cgc gat tgt tta 528
Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
165 170 175

att tca ggc ggt gat ggg ctg ctc atc aac gac caa att tta gaa tat 576
Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr

```

|   |     |     |      |
|---|-----|-----|------|
| 180   | 185 | 190 |      |
| att tta aaa gag ctg cgc agc att ccg cat ctg gaa gtc atc aga atc<br>Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile<br>195 | 200 | 205 | 624  |
| gga aca aga gct ccc gtc gtc ttt ccg cag cgc att acc gat cat ctg<br>Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu<br>210 | 215 | 220 | 672  |
| tgc gag ata ttg aaa aaa tat cat ccg gtc tgg ctg aac acc cat ttt<br>Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe<br>225 | 230 | 235 | 720  |
| aac aca agc atc gaa atg aca gaa tcc gtt gag gca tgt gaa aag<br>Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys<br>245     | 250 | 255 | 768  |
| ctg gtg aac gcg gga gtg ccg gtc gga aat cag gct gtc gta tta gca<br>Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala<br>260 | 265 | 270 | 816  |
| ggt att aat gat tcg gtt cca att atg aaa aag ctc atg cat gac ttg<br>Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu<br>275 | 280 | 285 | 864  |
| gta aaa atc aga gtc cgt cct tat tat att tac caa tgt gat ctg tca<br>Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser<br>290 | 295 | 300 | 912  |
| gaa gga ata ggg cat ttc aga gct cct gtt tcc aaa ggt ttg gag atc<br>Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile<br>305 | 310 | 315 | 960  |
| att gaa ggg ctg aga ggt cat acc tca ggc tat gcg gtt cct acc ttt<br>Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe<br>325 | 330 | 335 | 1008 |
| gtc gtt cac gca cca ggc gga gga ggt aaa atc gcc ctg cag ccg aac<br>Val Val His Ala Pro Gly Gly Lys Ile Ala Leu Gln Pro Asn<br>340         | 345 | 350 | 1056 |
| tat gtc ctg tca caa agt cct gac aaa gtg atc tta aga aat ttt gaa<br>Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu<br>355 | 360 | 365 | 1104 |
| ggt gtg att acg tca tat ccg gaa cca gag aat tat atc ccc aat cag<br>Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln<br>370 | 375 | 380 | 1152 |
| gca gac gcc tat ttt gag tcc gtt ttc cct gaa acc gct gac aaa aag<br>Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys<br>385 | 390 | 395 | 1200 |
| gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tcg ttt<br>Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe<br>405 | 410 | 415 | 1248 |
| aca cct gaa aat gta gac aga atc aaa agg aga gag gca tac atc gca<br>Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala<br>420 | 425 | 430 | 1296 |

aat ccg gag cat gaa aca tta aaa gat cgg cgt gag aaa aga gat cag 1344  
 Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln  
 435 440 445  
  
 ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act 1392  
 Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr  
 450 455 460  
  
 gaa tgc gga ggg gat tct tca tga 1416  
 Glu Cys Gly Gly Asp Ser Ser  
 465 470  
  
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 <211> 471  
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 <213> *Bacillus subtilis*  
  
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 Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu 1  
 1 5 10 15  
  
 Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
 20 25 30  
  
 Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
 35 40 45  
  
 Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
 50 55 60  
  
 Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
 65 70 75 80  
  
 Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met  
 85 90 95  
  
 His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp  
 100 105 110  
  
 Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
 115 120 125  
  
 Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg  
 130 135 140  
  
 Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
 145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr  
180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile  
195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu  
210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe  
225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys  
245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala  
260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu  
275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser  
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile  
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe  
325 330 335

Val Val His Ala Pro Gly Gly Lys Ile Ala Leu Gln Pro Asn  
340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu  
355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln  
370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys  
385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe

405

410

415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala  
 420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln  
 435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr  
 450 455 460

Glu Cys Gly Gly Asp Ser Ser  
 465 470

<210> 22  
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 <212> DNA  
 <213> Clostridium propionicum

<220>  
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 <222> (1) .. (438)  
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 Met Val Gly Lys Lys Val Val His His Leu Met Met Ser Ala Lys Asp  
 1 5 10 15  
 gct cac tat act gga aac tta gta aac ggc gct aga att gtg aat cag 96  
 Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln  
 20 25 30  
 tgg ggc gac gtt aca gaa tta atg gtt tat gtt gat ggt gac ata 144  
 Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile  
 35 40 45  
 agc tta ttc ttg ggc tac aaa gat atc gaa ttc aca gct cct gta tat 192  
 Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr  
 50 55 60  
 gtt ggt gac ttt atg gaa tac cac ggc ttg att gaa aaa gtt ggt aac 240  
 Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn  
 65 70 75 80  
 cag tcc tat aca tgt aaa ttt gaa gca ttg aaa gtt gca aca atg gtt 288  
 Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Thr Met Val  
 85 90 95  
 gat atc aca aat cct cag gat aca cgc gca aca gct tgt gag cct ccg 336  
 Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro  
 100 105 110  
 gta ttg tgc gga aga gca acg ggt agt ttg ttc atc gca aaa aaa gat 384  
 Val Leu Cys Gly Arg Ala Thr Gly Ser Leu Phe Ile Ala Lys Lys Asp

| 115   | 120 | 125 |   |
|---|-----|-----|---|
| cag aga ggc cct cag gaa tcc tct ttt aaa gag aga aag cac ccc ggt |     |     | 432   |
| Gln   | Arg | Gly | Pro Gln Glu Ser Ser Phe Lys Glu Arg Lys His Pro Gly |
| 130   |     | 135 | 140   |
| gaa tga   |     |     |   |
| Glu   |     |     | 438   |
| 145   |     |     |   |
| <210> 23  |     |     |   |
| <211> 145   |     |     |   |
| <212> PRT   |     |     |   |
| <213> Clostridium propionicum                                   |     |     |   |
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| Met Val Gly Lys Lys Val Val His His Leu Met Met Ser Ala Lys Asp |     |     |   |
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| Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln |     |     |   |
| 20  | 25  | 30  |   |
| Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile |     |     |   |
| 35  | 40  | 45  |   |
| Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr |     |     |   |
| 50  | 55  | 60  |   |
| Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn |     |     |   |
| 65  | 70  | 75  | 80  |
| Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Thr Met Val |     |     |   |
| 85  | 90  | 95  |   |
| Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro |     |     |   |
| 100   | 105 | 110 |   |
| Val Leu Cys Gly Arg Ala Thr Gly Ser Leu Phe Ile Ala Lys Lys Asp |     |     |   |
| 115   | 120 | 125 |   |
| Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Glu Arg Lys His Pro Gly |     |     |   |
| 130   | 135 | 140 |   |
| Glu   |     |     |   |
| 145   |     |     |   |
| <210> 24  |     |     |   |
| <211> 1554  |     |     |   |
| <212> DNA   |     |     |   |

&lt;213&gt; Megasphaera elsdenii

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1554)

&lt;223&gt;

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| <400> 24  |  |  |  |     |
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| Met Arg Lys Val Glu Ile Ile Thr Ala Glu Gln Ala Ala Gln Leu Val |  |  |  |     |
| 1 5 10 15   |  |  |  |     |
| aaa gac aac gac acg att acg tct atc ggc ttt gtc agc agc gcc cat |  |  |  | 96  |
| Lys Asp Asn Asp Thr Ile Thr Ser Ile Gly Phe Val Ser Ser Ala His |  |  |  |     |
| 20 25 30  |  |  |  |     |
| ccg gaa gca ctg acc aaa gct ttg gaa aaa cgg ttc ctg gac acg aac |  |  |  | 144 |
| Pro Glu Ala Leu Thr Lys Ala Leu Glu Lys Arg Phe Leu Asp Thr Asn |  |  |  |     |
| 35 40 45  |  |  |  |     |
| acc ccg cag aac ttg acc tac atc tat gca ggc tct cag ggc aaa cgc |  |  |  | 192 |
| Thr Pro Gln Asn Leu Thr Tyr Ile Tyr Ala Gly Ser Gln Gly Lys Arg |  |  |  |     |
| 50 55 60  |  |  |  |     |
| gat ggc cgt gcc gct gaa cat ctg gca cac aca ggc ctt ttg aaa cgc |  |  |  | 240 |
| Asp Gly Arg Ala Ala Glu His Leu Ala His Thr Gly Leu Leu Lys Arg |  |  |  |     |
| 65 70 75 80   |  |  |  |     |
| gcc atc atc ggt cac tgg cag act gta ccg gct atc ggt aaa ctg gct |  |  |  | 288 |
| Ala Ile Ile Gly His Trp Gln Thr Val Pro Ala Ile Gly Lys Leu Ala |  |  |  |     |
| 85 90 95  |  |  |  |     |
| gtc gaa aac aag att gaa gct tac aac ttc tcg cag ggc acg ttg gtc |  |  |  | 336 |
| Val Glu Asn Lys Ile Glu Ala Tyr Asn Phe Ser Gln Gly Thr Leu Val |  |  |  |     |
| 100 105 110   |  |  |  |     |
| cac tgg ttc cgc gcc ttg gca ggt cat aag ctc ggc gtc ttc acc gac |  |  |  | 384 |
| His Trp Phe Arg Ala Leu Ala Gly His Lys Leu Gly Val Phe Thr Asp |  |  |  |     |
| 115 120 125   |  |  |  |     |
| atc ggt ctg gaa act ttc ctc gat ccc cgt cag ctc ggc ggc aag ctc |  |  |  | 432 |
| Ile Gly Leu Glu Thr Phe Leu Asp Pro Arg Gln Leu Gly Gly Lys Leu |  |  |  |     |
| 130 135 140   |  |  |  |     |
| aat gac gta acc aaa gaa gac ctc gtc aaa ctg atc gaa gtc gat ggt |  |  |  | 480 |
| Asn Asp Val Thr Lys Glu Asp Leu Val Lys Leu Ile Glu Val Asp Gly |  |  |  |     |
| 145 150 155 160   |  |  |  |     |
| cat gaa cag ctt ttc tac ccg acc ttc ccg gtc aac gta gct ttc ctc |  |  |  | 528 |
| His Glu Gln Leu Phe Tyr Pro Thr Phe Pro Val Asn Val Ala Phe Leu |  |  |  |     |
| 165 170 175   |  |  |  |     |
| ccg ggt acg tat gct gat gaa tcc ggc aat atc acc atg gac gaa gaa |  |  |  | 576 |
| Arg Gly Thr Tyr Ala Asp Glu Ser Gly Asn Ile Thr Met Asp Glu Glu |  |  |  |     |
| 180 185 190   |  |  |  |     |
| atc ggg cct ttc gaa agc act tcc gta gcc cag gcc gtt cac aac tgt |  |  |  | 624 |
| Ile Gly Pro Phe Glu Ser Thr Ser Val Ala Gln Ala Val His Asn Cys |  |  |  |     |
| 195 200 205   |  |  |  |     |

|   |     |     |     |      |
|---|-----|-----|-----|------|
| ggc ggt aaa gtc gtc gtc cag gtc aaa gac gtc gtc gct cac ggc agc | 210 | 215 | 220 | 672  |
| Gly Gly Lys Val Val Val Gln Val Lys Asp Val Val Ala His Gly Ser |     |     |     |      |
| ctc gac ccg ccg atg gtc aag atc cct ggc atc tat gtc gac tac gtc | 225 | 230 | 235 | 720  |
| Leu Asp Pro Arg Met Val Lys Ile Pro Gly Ile Tyr Val Asp Tyr Val |     |     |     |      |
| gtc gta gca gct ccg gaa gac cat cag cag acg tat gac tgc gaa tac | 245 | 250 | 255 | 768  |
| Val Val Ala Ala Pro Glu Asp His Gln Gln Thr Tyr Asp Cys Glu Tyr |     |     |     |      |
| gat ccg tcc ctc agc ggt gaa cat cgt gct cct gaa ggc gct acc gat | 260 | 265 | 270 | 816  |
| Asp Pro Ser Leu Ser Gly Glu His Arg Ala Pro Glu Gly Ala Thr Asp |     |     |     |      |
| gca gct ctc ccc atg agc gct aag aaa atc atc ggc ccg ccg ggc gct | 275 | 280 | 285 | 864  |
| Ala Ala Leu Pro Met Ser Ala Lys Lys Ile Ile Gly Arg Arg Gly Ala |     |     |     |      |
| ttg gaa ttg act gaa aac gct gtc gtc aac ctc ggc gtc ggt gct ccg | 290 | 295 | 300 | 912  |
| Leu Glu Leu Thr Glu Asn Ala Val Val Asn Leu Gly Val Gly Ala Pro |     |     |     |      |
| gaa tac gtt gct tct gtt gcc ggt gaa gaa ggt atc gtc gat acc att | 305 | 310 | 315 | 960  |
| Glu Tyr Val Ala Ser Val Ala Gly Glu Gly Ile Ala Asp Thr Ile     |     |     |     |      |
| acc ctg acc gtc gaa ggt ggc gcc atc ggt ggc gta ccg cag ggc ggt | 325 | 330 | 335 | 1008 |
| Thr Leu Thr Val Glu Gly Ala Ile Gly Gly Val Pro Gln Gly Gly     |     |     |     |      |
| gcc cgc ttc ggt tcg tcc cgc aat gcc gat gcc atc atc gac cac acc | 340 | 345 | 350 | 1056 |
| Ala Arg Phe Gly Ser Ser Arg Asn Ala Asp Ala Ile Ile Asp His Thr |     |     |     |      |
| tat cag ttc gac ttc tac gat ggc ggc ggt ctg gac atc gct tac ctc | 355 | 360 | 365 | 1104 |
| Tyr Gln Phe Asp Phe Tyr Asp Gly Gly Leu Asp Ile Ala Tyr Leu     |     |     |     |      |
| ggc ctg gcc cag tgc gat ggc tcg ggc aac atc aac gtc agc aag ttc | 370 | 375 | 380 | 1152 |
| Gly Leu Ala Gln Cys Asp Gly Ser Gly Asn Ile Asn Val Ser Lys Phe |     |     |     |      |
| ggt act aac gtt gcc ggc tgc ggc ggt ttc ccc aac att tcc cag cag | 385 | 390 | 395 | 1200 |
| Gly Thr Asn Val Ala Gly Cys Gly Gly Phe Pro Asn Ile Ser Gln Gln |     |     |     |      |
| aca ccg aat gtt tac ttc tgc ggc acc ttc acg gct ggc ggc ttg aaa | 405 | 410 | 415 | 1248 |
| Thr Pro Asn Val Tyr Phe Cys Gly Thr Phe Thr Ala Gly Gly Leu Lys |     |     |     |      |
| atc gct gtc gaa gac ggc aaa gtc aag atc ctc cag gaa ggc aaa gcc | 420 | 425 | 430 | 1296 |
| Ile Ala Val Glu Asp Gly Lys Val Lys Ile Leu Gln Glu Gly Lys Ala |     |     |     |      |
| aag aag ttc atc aaa gct gtc gac cag atc act ttc aac ggt tcc tat | 435 | 440 | 445 | 1344 |
| Lys Lys Phe Ile Lys Ala Val Asp Gln Ile Thr Phe Asn Gly Ser Tyr |     |     |     |      |
| gca gcc ccg aac ggc aaa cac gtt ctc tac atc aca gaa ccg tgc gta |     |     |     | 1392 |

|   |     |     |      |
|---|-----|-----|------|
| Ala Ala Arg Asn Gly Lys His Val Leu Tyr Ile Thr Glu Arg Cys Val |     |     |      |
| 450   | 455 | 460 |      |
| ttt gaa ctg acc aaa gaa ggc ttg aaa ctc atc gaa gtc gca ccg ggc |     |     | 1440 |
| Phe Glu Leu Thr Lys Glu Gly Leu Lys Leu Ile Glu Val Ala Pro Gly |     |     |      |
| 465   | 470 | 475 | 480  |
| atc gat att gaa aaa gat atc ctc gct cac atg gac ttc aag ccg atc |     |     | 1488 |
| Ile Asp Ile Glu Lys Asp Ile Leu Ala His Met Asp Phe Lys Pro Ile |     |     |      |
| 485   | 490 | 495 |      |
| att gat aat ccg aaa ctc atg gat gcc cgc ctc ttc cag gac ggt ccc |     |     | 1536 |
| Ile Asp Asn Pro Lys Leu Met Asp Ala Arg Leu Phe Gln Asp Gly Pro |     |     |      |
| 500   | 505 | 510 |      |
| atg gga ctg aaa aaa taa   |     |     | 1554 |
| Met Gly Leu Lys Lys   |     |     |      |
| 515   |     |     |      |
| <210> 25  |     |     |      |
| <211> 517   |     |     |      |
| <212> PRT   |     |     |      |
| <213> Megasphaera elsdenii                                      |     |     |      |
| <400> 25  |     |     |      |
| Met Arg Lys Val Glu Ile Ile Thr Ala Glu Gln Ala Ala Gln Leu Val |     |     |      |
| 1   | 5   | 10  | 15   |
| Lys Asp Asn Asp Thr Ile Thr Ser Ile Gly Phe Val Ser Ser Ala His |     |     |      |
| 20  | 25  | 30  |      |
| Pro Glu Ala Leu Thr Lys Ala Leu Glu Lys Arg Phe Leu Asp Thr Asn |     |     |      |
| 35  | 40  | 45  |      |
| Thr Pro Gln Asn Leu Thr Tyr Ile Tyr Ala Gly Ser Gln Gly Lys Arg |     |     |      |
| 50  | 55  | 60  |      |
| Asp Gly Arg Ala Ala Glu His Leu Ala His Thr Gly Leu Leu Lys Arg |     |     |      |
| 65  | 70  | 75  | 80   |
| Ala Ile Ile Gly His Trp Gln Thr Val Pro Ala Ile Gly Lys Leu Ala |     |     |      |
| 85  | 90  | 95  |      |
| Val Glu Asn Lys Ile Glu Ala Tyr Asn Phe Ser Gln Gly Thr Leu Val |     |     |      |
| 100   | 105 | 110 |      |
| His Trp Phe Arg Ala Leu Ala Gly His Lys Leu Gly Val Phe Thr Asp |     |     |      |
| 115   | 120 | 125 |      |
| Ile Gly Leu Glu Thr Phe Leu Asp Pro Arg Gln Leu Gly Gly Lys Leu |     |     |      |
| 130   | 135 | 140 |      |

Asn Asp Val Thr Lys Glu Asp Leu Val Lys Leu Ile Glu Val Asp Gly  
145 150 155 160

His Glu Gln Leu Phe Tyr Pro Thr Phe Pro Val Asn Val Ala Phe Leu  
165 170 175

Arg Gly Thr Tyr Ala Asp Glu Ser Gly Asn Ile Thr Met Asp Glu Glu  
180 185 190

Ile Gly Pro Phe Glu Ser Thr Ser Val Ala Gln Ala Val His Asn Cys  
195 200 205

Gly Gly Lys Val Val Val Gln Val Lys Asp Val Val Ala His Gly Ser  
210 215 220

Leu Asp Pro Arg Met Val Lys Ile Pro Gly Ile Tyr Val Asp Tyr Val  
225 230 235 240

Val Val Ala Ala Pro Glu Asp His Gln Gln Thr Tyr Asp Cys Glu Tyr  
245 250 255

Asp Pro Ser Leu Ser Gly Glu His Arg Ala Pro Glu Gly Ala Thr Asp  
260 265 270

Ala Ala Leu Pro Met Ser Ala Lys Lys Ile Ile Gly Arg Arg Gly Ala  
275 280 285

Leu Glu Leu Thr Glu Asn Ala Val Val Asn Leu Gly Val Gly Ala Pro  
290 295 300

Glu Tyr Val Ala Ser Val Ala Gly Glu Glu Gly Ile Ala Asp Thr Ile  
305 310 315 320

Thr Leu Thr Val Glu Gly Gly Ala Ile Gly Gly Val Pro Gln Gly Gly  
325 330 335

Ala Arg Phe Gly Ser Ser Arg Asn Ala Asp Ala Ile Ile Asp His Thr  
340 345 350

Tyr Gln Phe Asp Phe Tyr Asp Gly Gly Leu Asp Ile Ala Tyr Leu  
355 360 365

Gly Leu Ala Gln Cys Asp Gly Ser Gly Asn Ile Asn Val Ser Lys Phe  
370 375 380

Gly Thr Asn Val Ala Gly Cys Gly Gly Phe Pro Asn Ile Ser Gln Gln  
 385 390 395 400

Thr Pro Asn Val Tyr Phe Cys Gly Thr Phe Thr Ala Gly Gly Leu Lys  
405 410 415

Ile Ala Val Glu Asp Gly Lys Val Lys Ile Leu Gln Glu Gly Lys Ala  
420 425 430

Lys Lys Phe Ile Lys Ala Val Asp Gln Ile Thr Phe Asn Gly Ser Tyr  
 435 440 445

Ala Ala Arg Asn Gly Lys His Val Leu Tyr Ile Thr Glu Arg Cys Val  
 450 455 . 460

Phe Glu Leu Thr Lys Glu Gly Leu Lys Leu Ile Glu Val Ala Pro Gly  
 465 470 475 480

Ile Asp Ile Glu Lys Asp Ile Leu Ala His Met Asp Phe Lys Pro Ile  
485 490 495

Ile Asp Asn Pro Lys Leu Met Asp Ala Arg Leu Phe Gln Asp Gly Pro  
500 505 510

Met Gly Leu Lys Lys  
515

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<210> 26
<211> 26
<212> DNA
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<220>  
<223> PCR primer

<400> 26  
caagctgggt ctgttcatgc tggatg

26

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<211> 27
<212> DNA
<213> Artificial Sequence
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<220> .  
<223> PCR primer

<400> 27  
aagcggttct cgccctcgta aacctga

27

<210> 28  
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<213> *Porphyromonas gingivalis*

<400> 28

Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu  
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Gln Trp Asn Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu  
20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly  
35 40 45

Val Lys Glu Ser Leu Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr  
50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln  
65 70 75 80

Ala Ile Pro Thr His Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val  
85 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His  
100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met  
115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala  
130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn  
145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu  
165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile  
180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu  
195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His  
210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu  
225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu  
245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val  
260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr  
275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr  
290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Glu Asn Leu Arg Gly His Thr  
305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly  
325 330 335

Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg  
340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu  
355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly  
370 375 380

Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala  
385 390 395 400

Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn  
405 410 415

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<213> *Porphyromonas gingivalis*

<220>  
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<222> (1)..(1251)  
<223>

<400> 29

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|---|-----|
| atg gca gaa agt cgt aga aag tat tat ttc cct gat gtc acc gat gag | 48  |
| Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu |     |
| 1 5 10 15   |     |
| caa tgg tac gac tgg cat tgg cag gtc ctc aat cga att gag acg ctc | 96  |
| Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu |     |
| 20 25 30  |     |
| gac cag ctg aaa aag tac gtt aca ctc acc gct gaa gaa gaa gag gga | 144 |
| Asp Gln Leu Lys Lys Tyr Val Thr Ala Glu Glu Glu Gly             |     |
| 35 40 45  |     |
| gta aaa gaa tcg ccc aaa gta ctc cga atg gct atc aca cct tat tat | 192 |
| Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr |     |
| 50 55 60  |     |
| ttg agt ttg ata gac ccc gag aat cct aat tgt ccg att cgt aaa caa | 240 |
| Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln |     |
| 65 70 75 80   |     |
| gcc att cct act caa cag gaa ctg gta cgt gct cct gaa gat cag gta | 288 |
| Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val |     |
| 85 90 95  |     |
| gac cca ctt agt gaa gat gaa gat tcg ccc gta ccc gga ctg act cat | 336 |
| Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His |     |
| 100 105 110   |     |
| cgt tat ccg gat cgt gta ttg ttc ctt atc acg gac aaa tgt tcg atg | 384 |
| Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met |     |
| 115 120 125   |     |
| tac tgt cgt cat tgt act cgc cgt cgc ttc gca gga cag aaa gat gct | 432 |
| Tyr Cys Arg His Cys Thr Arg Arg Phe Ala Gly Gln Lys Asp Ala     |     |
| 130 135 140   |     |
| tct tct cct gag cgc atc gat cga tgc att gac tat ata gcc aat     | 480 |
| Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn |     |
| 145 150 155 160   |     |
| aca ccg aca gtc cgc gat gtt ttg cta tcg gga ggc gat gcc ctc ctt | 528 |
| Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu |     |
| 165 170 175   |     |
| gtc agc gac gaa cgc ttg gaa tac ata ttg aag cgt ctg cgc gaa ata | 576 |
| Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile |     |
| 180 185 190   |     |
| cct cat gtg gag att gtt cgt ata gga agc cgt acg ccg gta gtc ctc | 624 |
| Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu |     |
| 195 200 205   |     |
| cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat | 672 |
| Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His |     |
| 210 215 220   |     |
| ccg gtg tgg ctg aac act cac ttc aac cac ccg aat gaa gtt acc gaa | 720 |
| Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu |     |
| 225 230 235 240   |     |

|   |      |
|---|------|
| gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg<br>Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu<br>245 250 255     | 768  |
| ggt aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg<br>Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val<br>260 265 270     | 816  |
| atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac<br>Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr<br>275 280 285     | 864  |
| tat ata tat gta tgc gat ctt tcg ctt gga ata ggt cat ttc cgc acg<br>Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr<br>290 295 300     | 912  |
| ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc<br>Pro Val Ser Lys Gly Ile Glu Ile Glu Asn Leu Arg Gly His Thr<br>305 310 315 320     | 960  |
| tcg ggc tat gca gtt cct acc ttt gtg gta ggt gct ccg ggg ggt ggt<br>Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly<br>325 330 335         | 1008 |
| ggt aag ata cct gta acg ccg aac tat gtt gta tct cag tcc cca cga<br>Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg<br>340 345 350     | 1056 |
| cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag<br>His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu<br>355 360 365     | 1104 |
| ccg gag aat tat cat gag gag tgc gat tgt gag gac tgt cga gcc ggt<br>Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly<br>370 375 380     | 1152 |
| aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct<br>Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala<br>385 390 395 400 | 1200 |
| atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac<br>Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn<br>405 410 415     | 1248 |
| tga   | 1251 |

<210> 30  
<211> 416  
<212> PRT  
<213> Porphyromonas gingivalis

<400> 30

Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu  
1 5 10 15

Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu  
20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Glu Gly  
 35 40 45

Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr  
 50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln  
 65 70 75 80

Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val  
 85 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His  
 100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met  
 115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala  
 130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn  
 145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu  
 165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile  
 180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu  
 195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His  
 210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu  
 225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu  
 245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val  
 260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr  
 275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr  
 290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Glu Asn Leu Arg Gly His Thr  
 305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly  
 325 330 335

Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg  
 340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu  
 355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly  
 370 375 380

Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala  
 385 390 395 400

Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn  
 405 410 415

<210> 31

<211> 471

<212> PRT

<213> Bacillus subtilis

<400> 31

Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu  
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Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
 20 25 30

Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
 35 40 45

Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
 50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
 65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met  
85 90 95

His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp  
100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
115 120 125

Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg  
130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr  
180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile  
195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu  
210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe  
225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys  
245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala  
260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu  
275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser  
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile  
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe  
 325 330 335

Val Val Asp Ala Pro Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn  
 340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu  
 355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln  
 370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys  
 385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe  
 405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala  
 420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln  
 435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr  
 450 455 460

Glu Cys Gly Gly Asp Ser Ser  
 465 470

<210> 32  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

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 cgcattcaag tcaaagacgt tcaggcta

28

<210> 33  
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 <213> Alcaligenes faecalis

<220>  
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 <222> (408) .. (1304)

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| gcaaaaccttc gccaaagggtg cgccctggttc ggctcggttg tcctttgagc tgctggagag | 120 |  |
| ggtgcatcac ctgtcttgg ccgatgttt ccgtctggaa tacattgtgt cgctgcaatg      | 180 |  |
| tggcgtacag ggcgacttcc aggaaggcat acgggcactg ctgattgata aagacaaaaca   | 240 |  |
| gccgcgctgg aatcctgcct cgctggaaaca ggcggatgca cgctgggtgg aacgttttt    | 300 |  |
| tgttcctgcc tggccggcag aaacgactca tccctggct gacctgtaac ccaggcagac     | 360 |  |
| cgctgcggcg ccagacggcg ccgcttcat aatgacgagg agacaaa atg agt aac       | 416 |  |
| Met Ser Asn  |     |  |
| 1  |     |  |
| acg att gca ttt atc ggg ctg ggc cat atg ggt aaa ccc atg gcg ctg      | 464 |  |
| Thr Ile Ala Phe Ile Gly Leu Gly His Met Gly Lys Pro Met Ala Leu      |     |  |
| 5 10 15  |     |  |
| aat ctg ctc aaa gcc ggt cat agc ctg aac gtc ttt gac ttg aat gcg      | 512 |  |
| Asn Leu Leu Lys Ala Gly His Ser Leu Asn Val Phe Asp Leu Asn Ala      |     |  |
| 20 25 30 35  |     |  |
| caa gcc atg cag gaa ctg cag gca gca ggg gca cag gtg ggg gaa tcg      | 560 |  |
| Gln Ala Met Gln Glu Leu Gln Ala Ala Gly Ala Gln Val Gly Glu Ser      |     |  |
| 40 45 50   |     |  |
| gcg gtg caa atc gcc caa gac gcg cag atg gtc ttt acc atg ctg cct      | 608 |  |
| Ala Val Gln Ile Ala Gln Asp Ala Gln Met Val Phe Thr Met Leu Pro      |     |  |
| 55 60 65   |     |  |
| gct ggc cgc cat gtt cgt cag gtt tac gag ggc gag aac ggc ttg ctg      | 656 |  |
| Ala Gly Arg His Val Arg Gln Val Tyr Glu Gly Glu Asn Gly Leu Leu      |     |  |
| 70 75 80   |     |  |
| cag act gtg gcc ccc ggt acg gtg ctg gtc gat tgc agc acc att gat      | 704 |  |
| Gln Thr Val Ala Pro Gly Thr Val Leu Val Asp Cys Ser Thr Ile Asp      |     |  |
| 85 90 95   |     |  |
| gcg caa acc agc cag gat ctg gcg gcc aaa gcc agc aag ctg ggt ctg      | 752 |  |
| Ala Gln Thr Ser Gln Asp Leu Ala Ala Lys Ala Ser Lys Leu Gly Leu      |     |  |
| 100 105 110 115  |     |  |
| ttc atg ctg gat gcg ccg gtc tcc ggt ggg acc ggt ggc gcc att gct      | 800 |  |
| Phe Met Leu Asp Ala Pro Val Ser Gly Gly Thr Gly Gly Ala Ile Ala      |     |  |
| 120 125 130  |     |  |
| ggc acc ttg acc ttt atg gtc ggg ggc gag gat cag gcc ctg gaa aag      | 848 |  |
| Gly Thr Leu Thr Phe Met Val Gly Gly Glu Asp Gln Ala Leu Glu Lys      |     |  |
| 135 140 145  |     |  |
| gcg cgc cct tac ttg gat gcc atg ggc aag aac att ttc cac gcg ggt      | 896 |  |
| Ala Arg Pro Tyr Leu Asp Ala Met Gly Lys Asn Ile Phe His Ala Gly      |     |  |
| 150 155 160  |     |  |
| aaa gcc ggt gcg ggt cag gtt gcc aag att tgc aac aat atg ctc ttg      | 944 |  |

|  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|
| Lys  | Ala | Gly | Ala | Gly | Gln | Val | Ala | Lys | Ile | Cys | Asn | Asn | Met | Leu | Leu  |     |
| 165  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| 170  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 175 |
| ggg att ttg atg gcg ggt act gct gaa gcc ttg gct ttg ggc gtt gcc  |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 992  |     |
| Gly  | Ile | Leu | Met | Ala | Gly | Thr | Ala | Glu | Ala | Leu | Ala | Leu | Gly | Val | Ala  |     |
| 180  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 195 |
| 185  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 190 |
| cac ggt ctg gac cct gcc gtg ctg tcg acc atc atg gcg cgc agt tcc  |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1040 |     |
| His  | Gly | Leu | Asp | Pro | Ala | Val | Leu | Ser | Thr | Ile | Met | Ala | Arg | Ser | Ser  |     |
| 200  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 210 |
| 205  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 210 |
| ggt cga aac tgg gca acc gag ctg tac aac ccc tgg cct ggg gtg atg  |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1088 |     |
| Gly  | Arg | Asn | Trp | Ala | Thr | Glu | Leu | Tyr | Asn | Pro | Trp | Pro | Gly | Val | Met  |     |
| 215  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 225 |
| 220  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 225 |
| ccg gat gta ccg gct tcg cgt gat tat cag ggc ggt ttt gcg acg ggc  |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1136 |     |
| Pro  | Asp | Val | Pro | Ala | Ser | Arg | Asp | Tyr | Gln | Gly | Gly | Phe | Ala | Thr | Gly  |     |
| 230  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 240 |
| 235  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 240 |
| ctg atg ctc aaa gac ctg ggt ctg gca gcc gat gcg gct gtc agc cag  |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1184 |     |
| Leu  | Met | Leu | Lys | Asp | Leu | Gly | Leu | Ala | Ala | Asp | Ala | Ala | Val | Ser | Gln  |     |
| 245  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 255 |
| 250  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 255 |
| aac agc gcg acg cct ttg ggc gaa ctg gca cgt aac ctg ttc gcc ttg  |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1232 |     |
| Asn  | Ser | Ala | Thr | Pro | Leu | Gly | Leu | Ala | Arg | Asn | Leu | Phe | Ala | Leu |      |     |
| 260  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 275 |
| 265  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 275 |
| cac gcc gca caa ggt cag aat gca ggg ctg gat ttc tcc agc att ctt  |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1280 |     |
| His  | Ala | Ala | Gln | Gly | Gln | Asn | Ala | Gly | Leu | Asp | Phe | Ser | Ser | Ile | Leu  |     |
| 280  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 290 |
| 285  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 290 |
| aat ttg tac cgt cag aag cac taa gttctggcag tgcgtagggc aggggctgca |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1334 |     |
| Asn  | Leu | Tyr | Arg | Gln | Lys | His |     |     |     |     |     |     |     |     |      |     |
| 295  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| gttccagcgc ctgtccttgc tccaaattgaa actggccttg ttccaggtcc gcc      |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1387 |     |
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| <212> PRT  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| <213> Alcaligenes faecalis                                       |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| <400> 34   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| Met Ser Asn Thr Ile Ala Phe Ile Gly Leu Gly His Met Gly Lys Pro  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| 1  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 15  |
|  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| Met Ala Leu Asn Leu Leu Lys Ala Gly His Ser Leu Asn Val Phe Asp  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| 20   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 30  |
|  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| Leu Asn Ala Gln Ala Met Gln Glu Leu Gln Ala Ala Gly Ala Gln Val  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| 35   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 45  |
|  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| Gly Glu Ser Ala Val Gln Ile Ala Gln Asp Ala Gln Met Val Phe Thr  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| 50   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      | 60  |
|  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |

Met Leu Pro Ala Gly Arg His Val Arg Gln Val Tyr Glu Gly Glu Asn  
65 70 75 80

Gly Leu Leu Gln Thr Val Ala Pro Gly Thr Val Leu Val Asp Cys Ser  
85 90 95

Thr Ile Asp Ala Gln Thr Ser Gln Asp Leu Ala Ala Lys Ala Ser Lys  
100 105 110

Leu Gly Leu Phe Met Leu Asp Ala Pro Val Ser Gly Gly Thr Gly Gly  
115 120 125

Ala Ile Ala Gly Thr Leu Thr Phe Met Val Gly Gly Glu Asp Gln Ala  
130 135 140

Leu Glu Lys Ala Arg Pro Tyr Leu Asp Ala Met Gly Lys Asn Ile Phe  
145 150 155 160

His Ala Gly Lys Ala Gly Ala Gly Gln Val Ala Lys Ile Cys Asn Asn  
165 170 175

Met Leu Leu Gly Ile Leu Met Ala Gly Thr Ala Glu Ala Leu Ala Leu  
180 185 190

Gly Val Ala His Gly Leu Asp Pro Ala Val Leu Ser Thr Ile Met Ala  
195 200 205

Arg Ser Ser Gly Arg Asn Trp Ala Thr Glu Leu Tyr Asn Pro Trp Pro  
210 215 220

Gly Val Met Pro Asp Val Pro Ala Ser Arg Asp Tyr Gln Gly Gly Phe  
225 230 235 240

Ala Thr Gly Leu Met Leu Lys Asp Leu Gly Leu Ala Ala Asp Ala Ala  
245 250 255

Val Ser Gln Asn Ser Ala Thr Pro Leu Gly Glu Leu Ala Arg Asn Leu  
260 265 270

Phe Ala Leu His Ala Ala Gln Gly Gln Asn Ala Gly Leu Asp Phe Ser  
275 280 285

Ser Ile Leu Asn Leu Tyr Arg Gln Lys His  
290 295

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cgacggatcc attcgtccgc ttgaataact aaag 34

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agagagcata tgtctttca ctttcggc 28

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39

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38

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38

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30

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32

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53

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ctagtctaga ggaaaccgct taacgaactc

30

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<213> Artificial Sequence

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54

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<212> DNA

<213> Artificial Sequence

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31

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gctataagaa tagcgattt a gctgaaagg gagacggac 39

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cgacggatcc gcagtgagtg agccttggag 30

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<220>
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Met Val Gly Lys Lys Val Val His His Leu Met Met Ser Ala Lys Asp
1 5 10 15

gct cac tat act gga aac tta gta aac ggc gct aga atc gtg aat cag 96
Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln
20 25 30

tgg ggc gac gta ggt aca gaa tta atg gtt tat gtt gat ggt gac atc 144
Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile
35 40 45

agc tta ttc ttg ggc tac aaa gat atc gaa ttc aca gct cct gta tat 192
Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr
50 55 60

gtt ggt gat ttt atg gaa tac cac ggc tgg att gaa aaa gtt ggc aac 240

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|   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val   | Gly | Asp | Phe | Met | Glu | Tyr | His | Gly | Trp | Ile | Glu | Lys | Val | Gly | Asn |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| cag tcc tat aca tgt aaa ttt gaa gca tgg aaa gta gca aag atg gtt |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 288 |  |
| Gln   | Ser | Tyr | Thr | Cys | Lys | Phe | Glu | Ala | Trp | Lys | Val | Ala | Lys | Met | Val |  |
|   |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |  |
| gat atc aca aat cca cag gat aca cgt gca aca gct tgt gaa cct ccg |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 336 |  |
| Asp   | Ile | Thr | Asn | Pro | Gln | Asp | Thr | Arg | Ala | Thr | Ala | Cys | Glu | Pro | Pro |  |
|   |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |  |
| gta ctt tgt ggt act gca aca ggc agc ctt ttc atc gca aag gat aat |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 384 |  |
| Val   | Leu | Cys | Gly | Thr | Ala | Thr | Gly | Ser | Leu | Phe | Ile | Ala | Lys | Asp | Asn |  |
|   |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |  |
| cag aga ggt cct cag gaa tct tcc aag gat gca aag cac cct caa     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 432 |  |
| Gln   | Arg | Gly | Pro | Gln | Glu | Ser | Ser | Phe | Lys | Asp | Ala | Lys | His | Pro | Gln |  |
|   |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |  |
| taa   |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 435 |  |
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| <213> Clostridium propionicum                                   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <400> 54  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Met   | Val | Gly | Lys | Lys | Val | Val | His | His | Leu | Met | Met | Ser | Ala | Lys | Asp |  |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|   |     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |  |
| Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|   |     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |  |
| Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|   |     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |  |
| Val   | Gly | Asp | Phe | Met | Glu | Tyr | His | Gly | Trp | Ile | Glu | Lys | Val | Gly | Asn |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Lys Met Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|   |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |  |
| Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|   |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |  |
| Val Leu Cys Gly Thr Ala Thr Gly Ser Leu Phe Ile Ala Lys Asp Asn |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|   |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |  |

Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Asp Ala Lys His Pro Gln  
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ctagtctaga tcaacgacca ctgaagttgg 30

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aaggaaaaaaaa gcggccgcctt taatatgcga tttggaggag 40

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ctagtctaga gcagtgagtg agccttggag 30

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cacacagaat tcattaaaga ggag

24

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cc 62

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ggaggggatt cttcatgaag taaggaggag atcttatatg gttgactttg agtttgatta 60

tg 62

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tcattcaccc gtgaggccat gaatatatct ccttcttaag ctttagtgctt ctgacggtag 60

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32